

GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2003, 16:41:42 ; Search time 56.5586 Seconds
(without alignments)
1362.510 Million cell updates/sec

Title: US-09-625-573-2
Perfect score: 1970
Sequence: 1 MLSTSRSRFRINTNESGEV.....GKGKSIGRAPEASLQDKEGA 374

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRMBL_21.*

1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	1252	63.6	352	6	Q95NC2		Q95nc2 callicebus
2	1244	63.1	339	6	Q9TUV8		Q9tuv8 saquinus sp
3	1244	63.1	339	6	Q9TQT3		Q9tgt3 callithrix
4	1244	63.1	339	6	Q9MZA0		Q9mza0 callithrix
5	1243	63.1	339	6	Q9TQV5		Q9tqv5 saquinus sp
6	1243	63.1	352	6	Q95NC4		Q95nc4 ateles geof
7	1240	62.9	339	6	Q9TUV0		Q9tuv0 saquinus sp
8	1239	62.9	352	6	Q9MZY9		Q9mzy9 ateles sp.
9	1238.5	62.9	339	6	Q9TUV6		Q9tuv6 saquinus sp
10	1238	62.8	339	6	Q9TUV1		Q9tuv1 saquinus sp
11	1237	62.8	339	6	Q9TUV9		Q9tuv9 saquinus sp
12	1236	62.7	339	6	Q9TQW0		Q9tqw0 hylobates c
13	1235	62.7	339	6	Q9TSN3		Q9tsn3 macaca fasc
14	1235	62.7	352	6	Q9T776		Q9t776 cercocobus
15	1234	62.6	339	6	Q9TUV5		Q9tuv5 saquinus sp
16	1233	62.6	339	6	Q9TUV2		Q9tuv2 alouatta ca

17	1233	62.6	352	6	Q95NE1		Q95nel cercocebus
18	1232	62.5	339	6	Q9TUX0		Q9tux0 hylobates c
19	1232	62.5	339	6	Q9TUV4		Q9tuv4 callithrix
20	1232	62.5	339	6	Q9TUV0		Q9tuv0 aotus trivi
21	1232	62.5	339	6	Q9TUV9		Q9tuv9 macaca mula
22	1231	62.5	339	6	Q9TUV9		Q9tuv9 hylobates c
23	1231	62.5	352	6	Q9XTI2		Q9xti2 cercopithec
24	1231	62.5	352	6	Q95NC9		Q95nc9 alouatta se
25	1231	62.5	352	6	Q95NC0		Q95nc0 hylobates m
26	1230	62.4	339	6	Q9TUV7		Q9tuv7 pan troglod
27	1230	62.4	339	6	Q9TUV7		Q9tuv7 macaca fusc
28	1230	62.4	339	6	Q9TUV5		Q9tuv5 macaca fusc
29	1230	62.4	339	6	Q9TUV4		Q9tuv4 macaca mula
30	1230	62.4	339	6	Q9TUV1		Q9tuv1 macaca mula
31	1230	62.4	339	6	Q9TQW4		Q9tqw4 pan troglod
32	1230	62.4	339	6	Q9TQW2		Q9tqw2 pongo pygma
33	1230	62.4	339	6	Q9TQT2		Q9tgt2 macaca neme
34	1230	62.4	339	6	Q9TQT1		Q9tgt1 macaca mula
35	1230	62.4	339	6	Q9TQT0		Q9tgt0 macaca fasc
36	1230	62.4	352	6	Q95NC5		Q95nc5 hylobates s
37	1230	62.4	352	6	Q97975		Q97975 macaca arc
38	1229	62.4	339	6	Q9TUV2		Q9tuv2 saquinus sp
39	1228	62.3	339	6	Q9TUV6		Q9tuv6 pan troglod
40	1228	62.3	339	6	Q9TQV6		Q9tqv6 colobus que
41	1228	62.3	339	6	Q9TQV3		Q9tqv3 cercopithec
42	1228	62.3	339	6	Q9TQV2		Q9tqv2 papio cynoc
43	1228	62.3	339	6	Q9TQR2		Q9tqr2 gorilla gor
44	1228	62.3	352	6	018770		018770 pan troglod
45	1228	62.3	352	6	Q9TV49		Q9tv49 cercocebus

ALIGNMENTS

RESULT 1

Q95NC2 PRELIMINARY; PRT; 352 AA.

AC Q95NC2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE C-C chemokine receptor 5.
GN CCR5.

OS Callicebus moloch (Dusky titi).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Callicebinae;
OC Callicebus.

OX NCBI_TaxID=9523;

RN [1]_TaxID=9523;

RP SEQUENCE FROM N.A.

RA Zhang Y., Ryder O.A., Zhang Y.;

RT "Sequence comparison of the CCR5 gene in primates and primate

RT phylogeny."

RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF177887; AAK4370.1;

DR InterPro: IPR000923; BlueCul.1.

DR InterPro: IPR000276; GPCR_Rhodpsn.

DR Pfam: PF00001; 7tm.1; 1.

DR PROSITE: PS00196; COPPER_BLUE; UNKNOWN_1.

DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.

DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.

KW Receptor.

SQ RECEPTOR. 352 AA; 40495 MW; 7FB307513ACF9B9B CRC64;

Query Match 63.6%; Score 1252; DB 6; Length 352;

Best Local Similarity 76.1%; Pred. No. 1.5e-102;

Matches 239; Conservative

Mismatches 26; Indels 12; Gaps 3;

OY 18 EVVTFEFDYDGA--PCHKFDVKQIGALLPPLYSLVFIFGVGNMLVLLINCKKLKC 75

Db 4 EVSSPIYDIDYGESEPCQKIDVKQMGALLPPLYSVMVFLFGVGNMLVLLINCKRUKS 63

OY 76 LTDIYLLNLAISDLFLITLPLWAHSAANEVWFGNMCKLFTGLYHIGYFGGFIILLT 135

Db	64	MTDIYLLNLAISSDLFFLTVFFWAHYAAGQWDGNTMCQFLTGLYIFGFSGFIITLT	123
Qy	136	IDRYLAIVHAVPALKARTVTFGVVTSVTWLVAVFAFASVPGIITKQCKEDSVVVCGPYP	195
Db	124	IDRYLAIVHAVFALKARTVTFGVVTSVTWVAVFAFSLPGIIFTRSQEGYHYTCSPHFP	183
Qy	196	RG-----WNNPHTTMRNLGLVLPLLLTWVICYSGILKTLRCRNEKRRHRAVVI	251
Db	184	FGYRFWKNELETLMWYLLGLVPLLVVWVICYSGILKTLRCRNEKRRHRAVRIIFTMIV	243
Qy	252	YFLFWPTNYIVLLNTFQBFEGFSLNCESQSDQATQVTTGLMTHCCINPIYAFVGEK	311
Db	244	YFLFWAPNYIVLLNTYQBFEGFLNCSNRLDQAMQVTTGLMTHCCVNPPIYAFVGEK	303
Qy	312	FRSLF-----HIA	319
Db	304	FRNYLLVFFOKHIA	317

RESULT 2	Q9TUV8	PRELIMINARY;	PRT;	339 AA.
ID	Q9TUV8			
AC	Q9TUV8;			
DT	01-MAY-2000 (TrEMBLrel. 13, Created)			
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)			
DE	C-C chemokine receptor 5 (Fragment).			
GN	CCR5			
OS	Saguinus sp.			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.			
OX	NCBI_TaxID=100754;			
LN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Kunshan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,			
RA	Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;			
RT	"Sequences of the CCR5 genes from diverse simian and prosimian			
RT	species";			
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF161529; AAD47686.1; -			
DR	InterPro; IPR000923; BlueCu_1.			
DR	InterPro; IPR000276; GPCR_Rhodpsn.			
DR	Pfam; PF00001; 7tm.1; 1.			
DR	PRINTS; PR00237; GPCRHHODPSN.			
DR	PROSITE; PS00196; COPPER.BLUE; UNKNOWN_1.			
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.			
DR	PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.			
DR	Receptor.			
FT	NON_TER	1		
FT	NON_TER	339		
SEQ	SEQUENCE	339 AA;	39164 MW;	6A67CF5D22C70C49 CRC64;

QY	258	PYNIVILLNTQOEFGLNSCESTSQLODAQTVTETLGMTHCCINPIIYAFVGEKFRSLF-	316
Db	243	PYNIVILLNTQOEFGLNCSSSNRLDQAMQVETETLGMTHCCINPIIYAFVGEKFRNVL	302
QY	317	-----HIA 319	
Db	303	VFFQKHIA 310	
RESULT 3			
Q9TQ73			
ID	Q9TQ73	PRELIMINARY;	PRT; 339 AA.
AC	Q9TQ73;		
DC	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-MAY-2002 (TREMBLrel. 20, Last annotation update)		
DE	C-C chemokine receptor 5 (Fragment).		
GN	CCR5.		
OS	Callithrix jacchus (Common marmoset).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix		
OX	NCBI_TaxID=9483;		
RN	[1]		

Query Match	63.1%;	Score 1244;	DB 6;	Length 339;
Best Local Similarity	77.3%;	Pred. No. 7.3e-102;		
Matches 238;	Conservative 24;	Mismatches 34;	Indels 12;	Gaps
24 QY	FDYDYG--APCHKE	DVKYQAGQLLP	LSIVFTFGVGNMLV	LLINCKKLC
24 dbb				
3 QY	YDIDYG	SEPCRKIDKQ	GAHLLLP	YSWVFGVGNMLV
3 dbb				
82 QY	LNLAISDL	FLFLTLPLWAH	SAANEWVFGN	AMCKLFTGLX
82 dbb				
63 QY	LNLAISDL	FLFLTVFPWA	HYAAGQWDFG	NMCQFLTGLY
63 dbb				
142 QY	IYHVFALK	ARVTTCGV	TSVITLWAV	FPASVPGI
142 dbb				
123 QY	IYHVFALK	ARVTTCGV	TSVITLWAV	FPASVPGI
123 dbb				
198 QY	WNFFIT	IMRNILGLV	PLLIWICYS	GIILTKLLRC
198 dbb				
193 QY	WKNFET	LKMWILGLV	PLLIWICYS	GIILTKLLRC
193 dbb				

[illegible]

QY 317 -----HIA 319
 Db 303 VFFQKHIA 310

RESULT 4

Q9MZA0 ID Q9MZA0 PRELIMINARY; PRT; 352 AA.
 AC Q9MZA0;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE CC chemokine receptor 5 (C-C chemokine receptor 5).
 GN CCR5.
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
 OX NCBI_TaxID=9483;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20317091; PubMed=10747879;
 RX Mummidi S., Banskad M., Ahuja S.S., Gonzalez E., Feuillet P.M.,
 RA Begum K., Galvis M.C., Kosteki V., Valente A.J., Murthy K.K.,
 RA "Evolution of human and non-human primate CC chemokine receptor 5 gene
 RT and mRNA. Potential roles for haplotype and mRNA diversity,
 RT differential haplotype-specific transcriptional activity, and altered
 RT transcription factor binding to polymorphic nucleotides in the
 RT pathogenesis of HIV-1 and simian immunodeficiency virus.";
 RL J. Biol. Chem. 275:18946-18961(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Ryder O.A., Zhang Y.;
 RA "Sequence comparison of the CCR5 gene in primates and primate
 RT phylogeny.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF252554; AAF87984.1; -;
 DR EMBL: AF177878; AAK43361.1; -;
 DR InterPro: IPR000923; BlueCu1.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00196; COPPER_BLUE; UNKNOWN_1.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
 DR PROSITE: PS00262; G_PROTEIN_RECEP_FL_2; 1.
 KW Receptor.
 SQ SEQUENCE 352 AA; 40465 MW; FF0D0A8D06F7B8F5 CRC64;
 Query Match 63.1%; Score 1244; DB 6; Length 352;
 Best Local Similarity 76.6%; Pred. No. 7.5e-102;
 Matches 236; Conservative 27; Mismatches 33; Indels 12; Gaps 3;
 QY 24 FDYDYG--APCHKFDVKQIGAOQLLPPLYSLVFIFGVGNMLVLLINCKKLCLTDIYL 81
 Db 10 YDIDYGPSEPCRKIDVQKMGHALLPPLYSMLVFLGVGNMLVLLINCKKLKSMTDIYL 69
 QY 82 LNLAISDLFLTLPLWAHSAANEVFGNACKLFTGLYHIGYFGGIFILLTIDRYLA 141
 Db 70 LNLAISDLFLTLPLWAHSAANEVFGNACKLFTGLYHIGYFGGIFILLTIDRYLA 129
 QY 142 IVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTKCKEDSVYVCGPYPRG---RG 197
 Db 130 IVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTKCKEDSVYVCGPYPRG---RG 189
 QY 198 WNNFHTIMRNILGLVPLLMVICYSGILKTLRLCRNEKKRRHRAVRVFTIMIVFLFWT 257
 Db 190 WNNFHTIMRNILGLVPLLMVICYSGILKTLRLCRNEKKRRHRAVRVFTIMIVFLFWA 249
 QY 258 PYNIVILLNTFOEFFGLSNCSTESOLDQATQVTEITLGMTHCCINPIIYAFVGEKFRSLF- 316
 Db 250 PYNIVILLNTFOEFFGLSNCSTESOLDQATQVTEITLGMTHCCINPIIYAFVGEKFRSLF- 309

QY 317 -----HIA 319
 Db 310 VFFQKHIA 317

RESULT 5

Q9TQV5 ID Q9TQV5 PRELIMINARY; PRT; 339 AA.
 AC Q9TQV5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE CC chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Sagulnus.
 OX NCBI_TaxID=100754;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF161931; AAD47688.1; -;
 DR EMBL: AF161923; AAD47680.1; -;
 DR EMBL: AF161925; AAD47682.1; -;
 DR EMBL: AF161926; AAD47683.1; -;
 DR InterPro: IPR000923; BlueCu1.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00196; COPPER_BLUE; UNKNOWN_1.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
 DR PROSITE: PS00262; G_PROTEIN_RECEP_FL_2; 1.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 39081 MW; 6B79D05D22C70032 CRC64;
 Query Match 63.1%; Score 1243; DB 6; Length 339;
 Best Local Similarity 76.9%; Pred. No. 8.9e-102;
 Matches 237; Conservative 25; Mismatches 34; Indels 12; Gaps 3;
 QY 24 FDYDYG--APCHKFDVKQIGAOQLLPPLYSLVFIFGVGNMLVLLINCKKLCLTDIYL 81
 Db 3 YDIDYGPSEPCRKIDVQKMGHALLPPLYSMLVFLGVGNMLVLLINCKKRKSMTDIYL 62
 QY 82 LNLAISDLFLTLPLWAHSAANEVFGNACKLFTGLYHIGYFGGIFILLTIDRYLA 141
 Db 63 LNLAISDLFLTLPLWAHSAANEVFGNACKLFTGLYHIGYFGGIFILLTIDRYLA 122
 QY 142 IVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTKCKEDSVYVCGPYPRG--- 197
 Db 123 IVHAVFALKARTVTFGVVTSVITLWVAVFASVPGIIFTKCKEDSVYVCGPYPRG--- 182
 QY 198 WNNFHTIMRNILGLVPLLMVICYSGILKTLRLCRNEKKRRHRAVRVFTIMIVFLFWT 257
 Db 183 WNNFHTIMRNILGLVPLLMVICYSGILKTLRLCRNEKKRRHRAVRVFTIMIVFLFWA 242
 QY 258 PYNIVILLNTFOEFFGLSNCSTESOLDQATQVTEITLGMTHCCINPIIYAFVGEKFRSLF- 316
 Db 243 PYNIVILLNTFOEFFGLSNCSTESOLDQATQVTEITLGMTHCCINPIIYAFVGEKFRSLF- 302
 QY 317 -----HIA 319
 Db 303 VFFQKHIA 310

RESULT 6

Q95NC4 ID Q95NC4 PRELIMINARY; PRT; 352 AA.

DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_FL_2; 1.
 KW Receptor.
 SQ SEQUENCE 352 AA; 40471 MW; 01E397C2A87DE64D CRC64;
 Query Match 62.9%; Score 1239; DB 6; Length 352;
 Best Local Similarity 76.3%; Pred. No. 2.1e-101;
 Matches 235; Conservative 27; Mismatches 34; Indels 12; Gaps 3;
 QY 24 FDYDYG--APCHKEDVKOIGAQQLPPLYSLVFIQGVGNMVLVLLINCKKLCITDIYL 81
 Db 10 YDIDYGPSEPCRKIDVKQGAHLLPPLYSWVFLFQGVGNMVLVLLINCKKRPKSTDIYL 69
 QY 82 LNLAISDLLFLITLPLWAHSAANWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
 Db 70 LNLTSIDLLFLFTVFWAHYAAGQWDFGNTMCQFLTGLYFGFFSGIFFIILLTIDRYLA 129
 QY 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFPRG--- 197
 Db 130 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTRSQEGVHYTCSPHFPQYQF 189
 QY 198 WNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKKRHRVAVRFTIMIVFLEWFT 257
 Db 190 WNFETLKMVILGLVPLLMVICYSGILKTLRCRNEKKRHRVAVRFTIMIVFLEWFA 249
 QY 258 PYNIVILLNTFOEFFGLSNCESTSQLDQATQVETLGMTHCCINPIIYAFVGEKFRSLP- 316
 Db 250 PYNIVILLNTYQEFFGLNCSNRLDQAMQVETLGMTHCCVNPPIIYAFVGEKFRNYLL 309
 QY 317 -----HIA 319
 Db 310 VFFQKHIA 317

RESULT 9
 Q9TUV6 PRELIMINARY; PRT; 339 AA;
 ID Q9TUV6
 AC Q9TUV6
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Saguinus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
 OX NCBI_TaxID=100754;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161932; AAD47689.1; -
 DR InterPro; IPR000923; BlueCu.1.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_FL_2; 1.
 KW Receptor.
 FT NON_TER
 FT SEQUENCE 339 AA; 38993 MW; 0559F4F0FEC70F5F CRC64;
 Query Match 62.9%; Score 1238.5; DB 6; Length 339;
 Best Local Similarity 75.3%; Pred. No. 2.2e-101;
 Matches 236; Conservative 26; Mismatches 43; Indels 9; Gaps 3;

QY 24 FDYDYG--APCHKEDVKOIGAQQLPPLYSLVFIQGVGNMVLVLLINCKKLCITDIYL 81
 Db 3 YDIDYGPSEPCRKIDVKQGAHLLPPLYSWVFLFQGVGNMVLVLLINCKKRPKSTDIYL 62
 QY 82 LNLAISDLLFLITLPLWAHSAANWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
 Db 63 LNLTSIDLLFLFTVFWAHYAAGQWDFGNTMCQFLTGLYFGFFSGIFFIILLTIDRYLA 122
 QY 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFPRG--- 197
 Db 133 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTRSQEGVHYTCSPHFPQYQF 182
 QY 198 WNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKKRHRVAVRFTIMIVFLEWFT 257
 Db 183 WNFETLKMVILGLVPLLMVICYSGILKTLRCRNEKKRHRVAVRFTIMIVFLEWFA 242
 QY 258 PYNIVILLNTFOEFFGLSNCESTSQLDQATQVETLGMTHCCINPIIYAFVGEKFRSLP 317
 Db 243 PYNIVILLNTYQEFFGLNCSNRLDQAMQVETLGMTHCCVNPPIIYAFVGEKFRNYL 302
 QY 318 IALGCKRIAPLOKPVCG 333
 Db 303 VFFQKHIA--KQFCG 315
 RESULT 10
 Q9TUM1 PRELIMINARY; PRT; 339 AA;
 ID Q9TUM1
 AC Q9TUM1
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Saguinus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
 OX NCBI_TaxID=100754;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161924; AAD47681.1; -
 DR InterPro; IPR000923; BlueCu.1.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_FL_2; 1.
 KW Receptor.
 FT NON_TER
 FT SEQUENCE 339 AA; 39069 MW; 5146237770BC70028 CRC64;
 Query Match 62.8%; Score 1238; DB 6; Length 339;
 Best Local Similarity 76.6%; Pred. No. 2.5e-101;
 Matches 236; Conservative 25; Mismatches 35; Indels 12; Gaps 3;
 QY 24 FDYDYG--APCHKEDVKOIGAQQLPPLYSLVFIQGVGNMVLVLLINCKKLCITDIYL 81
 Db 3 YDIDYGPSEPCRKIDVKQGAHLLPPLYSWVFLFQGVGNMVLVLLINCKKRPKSTDIYL 62
 QY 82 LNLAISDLLFLITLPLWAHSAANWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
 Db 63 LNLTSIDLLFLFTVFWAHYAAGQWDFGNTMCQFLTGLYFGFFSGIFFIILLTIDRYLA 122
 QY 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVYVCGPYFPRG--- 197
 Db 123 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTRSQEGVHYTCSPHFPQYQF 182

```

QY 198 WNNFHTIMRNILGLVPLLLIMVICYSGILKTLRCRNEKKRRAVRVIFTIMIVFLFWT 257
DB 183 WKNFETLKMVLGLVPLLLIMVICYSGILKTLRCRNEKKRRAVRVIFTIMIVFLFWA 242
QY 258 PYNIVILLNTQOEFGNLSNCESTOLDQATQVETLGMTHCCINPIIYAFVGEKFRSLF- 316
DB 243 PYNIVILLNTQOEFGNLSNCESTOLDQATQVETLGMTHCCINPIIYAFVGEKFRSLF- 302
QY 317 -----HIA 319
DB 303 VFFQKHIA 310

RESULT 11
Q9TUV9 ID Q9TUV9 PRELIMINARY; PRT; 339 AA.
AC Q9TUV9
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Saguinus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=100754;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161928; AAD47685.1;
DR InterPro; IPR000923; BlueCu.1.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 6633F6022C71P0F CRC64;

Query Match 62.8%; Score 1237; DB 6; Length 339;
Best Local Similarity 76.6%; Pred. No. 3e-101;
Matches 236; Conservative 25; Mismatches 35; Indels 12; Gaps 3;

QY 24 FDYDYG--APCHKFDVKQIGAOQLPPLYSIVFTFGVGNMVLVILINCKKLKCLTDIYL 81
DB 3 YDIDYGPSPCKIDVKQGAHLPLPLYSIVFTFGVGNMVLVILINCKKLKCLTDIYL 62
QY 82 LNAISDLLFLTLPLWAHSAANEWFGNAMKLTGLYHIGYFGGFIILLTIDRYLA 141
DB 63 LNAISDLIFLTVPFWAHYAAGQWDFGNTMCQFLTGLYFGGFIILLTIDRYLA 122
QY 142 IVHAVFALKARTVTFGVTSVITLWVAVFASVPGIIFTKCKEDSVYVCGPYPRG---- 197
DB 123 IVHAVFALKARTVTFGVTSVITLWVAVFASVPGIIFTKCKEDSVYVCGPYPRG---- 182
QY 198 WNNFHTIMRNILGLVPLLLIMVICYSGILKTLRCRNEKKRRAVRVIFTIMIVFLFWT 257
DB 183 WKNFETLKMVLGLVPLLLIMVICYSGILKTLRCRNEKKRRAVRVIFTIMIVFLFWA 242
QY 258 PYNIVILLNTQOEFGNLSNCESTOLDQATQVETLGMTHCCINPIIYAFVGEKFRSLF- 316
DB 243 PYNIVILLNTQOEFGNLSNCESTOLDQATQVETLGMTHCCINPIIYAFVGEKFRSLF- 302
QY 317 -----HIA 319
DB 303 VFFQKHIA 310

RESULT 12
Q9TOWO ID Q9TOWO PRELIMINARY; PRT; 339 AA.
AC Q9TOWO
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162024; AAD47779.1;
DR EMBL; AF161889; AAD47646.1;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 5555FEAF2614D35C CRC64;

Query Match 62.7%; Score 1236; DB 6; Length 339;
Best Local Similarity 77.4%; Pred. No. 3.7e-101;
Matches 236; Conservative 25; Mismatches 34; Indels 10; Gaps 2;

QY 25 DYDYGAPCHKFDVKQIGAOQLPPLYSIVFTFGVGNMVLVILINCKKLKCLTDIYL 84
DB 6 DYTSEPCQKINVKQIAARLLPPLYSIVFTFGVGNMVLVILINCKKLKCLTDIYL 65
QY 85 AISDLLFLTLPLWAHSAANEWFGNAMKLTGLYHIGYFGGFIILLTIDRYLAIVH 144
DB 66 AISDLFELLTVPFWAHYAAGQWDFGNTMCQFLTGLYFGGFIILLTIDRYLAIVH 125
QY 145 AVFALKARTVTFGVTSVITLWVAVFASVPGIIFTKCKEDSVYVCGPYPRP----RGWNN 200
DB 126 AVFALKARTVTFGVTSVITLWVAVFASVPGIIFTKCKEDSVYVCGPYPRP---- 185
QY 201 FHTIMRNILGLVPLLLIMVICYSGILKTLRCRNEKKRRAVRVIFTIMIVFLFWT 260
DB 186 FQTLKIVILGLVPLVLMVICYSGILKTLRCRNEKKRRAVRVIFTIMIVFLFWAPYN 245
QY 261 IVLLNTQOEFGNLSNCESTOLDQATQVETLGMTHCCINPIIYAFVGEKFRSLF---- 316
DB 246 IVLLNTQOEFGNLSNCESTOLDQATQVETLGMTHCCINPIIYAFVGEKFRSLF---- 305
QY 317 --HIA 319
DB 306 QKHIA 310

RESULT 13
Q9TSN3 ID Q9TSN3 PRELIMINARY; PRT; 339 AA.
AC Q9TSN3
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.

```

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF161951; AAD47707.1; -;
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHHODOPS.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 1 339
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 3908 MW; F0132E8BC44EFB29 CRC64;
 Query Match 62.7%; Score 1235; DB 6; Length 339;
 Best Local Similarity 77.3%; Pred. No. 4.5e-101;
 Matches 238; Conservative 25; Mismatches 33; Indels 12; Gaps 3;
 QY 24 FDYDY--GAPCHFDVQKIGQAQLLPPLYSILVIFGFGVGNMLVLLINCKLKCLTDIYL 81
 Db 3 YDIDYTSQPCQKINVKQIAARLLPPLYSILVIFGFGVGNMLVLLINCKLKCLTDIYL 62
 QY 82 LNLAISDLLEFLITLPLWAHSAANEWFGNAMCKLTGLYHIGYFGGFIFFILLTIDRYLA 141
 Db 63 LNLAISDLLEFLITLPLWAHSAANEWFGNAMCKLTGLYHIGYFGGFIFFILLTIDRYLA 122
 QY 142 IVHAFVFAKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVVCGPYFP---RG 197
 Db 123 IVHAFVFAKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVVCGPYFP---RG 182
 QY 198 WNNPHTTMRNLGLVPLLMVICYSGLIKTLRCRNEKKRHRVAVLFTIMIVYFLFWT 257
 Db 183 WKNFQTLKIVLGLVPLLMVICYSGLIKTLRCRNEKKRHRVAVLFTIMIVYFLFWA 242
 QY 258 PYNIVILLNTOEFEGFLNSCESTSQLDQATQVETLGMTHCCINPIIYAFVGEKFRSLF- 316
 Db 243 PYNIVILLNTOEFEGFLNSCESTSQLDQATQVETLGMTHCCINPIIYAFVGEKFRNVL 302
 QY 317 -----HIA 319
 Db 303 VFFQKHIA 310
 RESULT 14
 O77776 PRELIMINARY; PRT; 352 AA.
 ID O77776
 AC O77776;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE C-C chemokine receptor CCR5.
 GN CCR5.
 OS Cercocebus torquatus torquatus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Cercocebus.
 OX NCBI_TaxID=81944;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1208;
 RA Chen Z., Kwon D., Jin Z., Monard S., Telfer P., Jones M., Lu C.,
 RA Aguilar R., Ho D.D., Marx P.A.;
 RT "Natural infection of a homozygous delta 24 CCR5 red-capped mangabey
 with a R2b-tropic simian immunodeficiency virus.";

J. Exp. Med. 0:0-0(1998).
 EMBL: AF084004; AAC62472.1; -;
 InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHHODOPS.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 352 AA; 40475 MW; B3A63FDC4473D1D3 CRC64;
 Query Match 62.7%; Score 1235; DB 6; Length 352;
 Best Local Similarity 76.9%; Pred. No. 4.7e-101;
 Matches 237; Conservative 27; Mismatches 32; Indels 12; Gaps 3;
 QY 24 FDYDY--GAPCHFDVQKIGQAQLLPPLYSILVIFGFGVGNMLVLLINCKLKCLTDIYL 81
 Db 10 YDIDYTSQPCQKINVKQIAARLLPPLYSILVIFGFGVGNMLVLLINCKLKCLTDIYL 69
 QY 82 LNLAISDLLEFLITLPLWAHSAANEWFGNAMCKLTGLYHIGYFGGFIFFILLTIDRYLA 141
 Db 70 LNLAISDLLEFLITLPLWAHSAANEWFGNAMCKLTGLYHIGYFGGFIFFILLTIDRYLA 129
 QY 142 IVHAFVFAKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVVCGPYFP---RG 197
 Db 130 IVHAFVFAKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVVCGPYFP---RG 189
 QY 198 WNNPHTTMRNLGLVPLLMVICYSGLIKTLRCRNEKKRHRVAVLFTIMIVYFLFWT 257
 Db 190 WKNFQTLKIVLGLVPLLMVICYSGLIKTLRCRNEKKRHRVAVLFTIMIVYFLFWA 249
 QY 258 PYNIVILLNTOEFEGFLNSCESTSQLDQATQVETLGMTHCCINPIIYAFVGEKFRSLF- 316
 Db 250 PYNIVILLNTOEFEGFLNSCESTSQLDQATQVETLGMTHCCINPIIYAFVGEKFRNVL 309
 QY 317 -----HIA 319
 Db 310 VFFQKHIA 317
 RESULT 15
 Q9TUV5 PRELIMINARY; PRT; 339 AA.
 ID Q9TUV5
 AC Q9TUV5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20; Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Saguinus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
 OX NCBI_TaxID=100754;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF161933; AAD47690.1; -;
 DR InterPro: IPR000923; BlueCu.1.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHHODOPS.
 DR PROSITE: PS00196; COPPER_BLUE; UNKNOWN_1.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 1 339
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 39021 MW; 8DACBD0D6C785073 CRC64;
 Query Match 62.6%; Score 1234; DB 6; Length 339;

